SEQUENCE LISTING

<110> Rosanne M. Crooke
Mark J. Graham
Kristina M. Lemonidis

<120> ANTISENSE MODULATION OF ACYL COENZYME A CHOLESTEROL ACYLTRANSFERASE-1 EXPRESSION

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Thr Leu Ser Ala Ser Ala Ala Trp Gly Ala His Pro Ser Ser Pro Pro
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Val Val Asp Thr Val His Gly Lys Val Leu Gly Lys Phe Val Ser Leu
30 35 40

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gaa gga ttt gca cag cct gtg gcc att ttc ctg gga atc cct ttt gcc   198
Glu Gly Phe Ala Gln Pro Val Ala Ile Phe Leu Gly Ile Pro Phe Ala
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aag ccg cct ctt gga ccc ctg agg ttt act cca ccg cag cct gca gaa   246
Lys Pro Pro Leu Gly Pro Leu Arg Phe Thr Pro Pro Gln Pro Ala Glu
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cca tgg agc ttt gtg aag aat gcc acc tcg tac cct cct atg tgc acc   294
Pro Trp Ser Phe Val Lys Asn Ala Thr Ser Tyr Pro Pro Met Cys Thr
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caa gat ccc aag gcg ggg cag tta ctc tca gag cta ttt aca aac cga   342
Gln Asp Pro Lys Ala Gly Gln Leu Leu Ser Glu Leu Phe Thr Asn Arg
90                  95                  100                 105

aag gag aac att cct ctc aag ctt tct gaa gac tgt ctt tac ctc aat   390
Lys Glu Asn Ile Pro Leu Lys Leu Ser Glu Asp Cys Leu Tyr Leu Asn
                110                 115                 120

att tac act cct gct gac ttg acc aag aaa aac agg ctg ccg gtg atg   438
Ile Tyr Thr Pro Ala Asp Leu Thr Lys Lys Asn Arg Leu Pro Val Met
            125                 130                 135

gtg tgg atc cac gga ggg ggg ctg atg gtg ggt gcg gca tca acc tat   486
Val Trp Ile His Gly Gly Gly Leu Met Val Gly Ala Ala Ser Thr Tyr
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gat ggg ctg gcc ctt gct gcc cat gaa aac gtg gtg gtg gtg acc att   534
Asp Gly Leu Ala Leu Ala Ala His Glu Asn Val Val Val Val Thr Ile
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caa tat cgc ctg ggc atc tgg gga ttc ttc agc aca ggg gat gaa cac   582
Gln Tyr Arg Leu Gly Ile Trp Gly Phe Phe Ser Thr Gly Asp Glu His
170                 175                 180                 185

agc cgg ggg aac tgg ggt cac ctg gac cag gtg gct gcc ctg cgc tgg   630
Ser Arg Gly Asn Trp Gly His Leu Asp Gln Val Ala Ala Leu Arg Trp
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Val Gln Asp Asn Ile Ala Ser Phe Gly Gly Asn Pro Gly Ser Val Thr
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atc ttt gga gag tca gcg gga gga gaa agt gtc tct gtt ctt gtt ttg   726
Ile Phe Gly Glu Ser Ala Gly Gly Glu Ser Val Ser Val Leu Val Leu
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tct cca ttg gcc aag aac ctc ttc cac cgg gcc att tct gag agt ggc   774
Ser Pro Leu Ala Lys Asn Leu Phe His Arg Ala Ile Ser Glu Ser Gly
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gtg gcc ctc act tct gtt ctg gtg aag aaa ggt gat gtc aag ccc ttg   822
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Val Met Val His Cys Leu Arg Gln Lys Thr Glu Glu Glu Leu Leu Glu
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acg aca ttg aaa atg aaa ttc tta tct ctg gac tta cag gga gac ccc   966
Thr Thr Leu Lys Met Lys Phe Leu Ser Leu Asp Leu Gln Gly Asp Pro
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aga gag agt caa ccc ctt ctg ggc act gtg att gat ggg atg ctg ctg   1014
Arg Glu Ser Gln Pro Leu Leu Gly Thr Val Ile Asp Gly Met Leu Leu
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ctg aaa aca cct gaa gag ctt caa gct gaa agg aat ttc cac act gtc   1062
Leu Lys Thr Pro Glu Glu Leu Gln Ala Glu Arg Asn Phe His Thr Val
330                 335                 340                 345

ccc tac atg gtc gga att aac aag cag gag ttt ggc tgg ttg att cca   1110
Pro Tyr Met Val Gly Ile Asn Lys Gln Glu Phe Gly Trp Leu Ile Pro
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atg cag ttg atg agc tat cca ctc tcc gaa ggg caa ctg gac cag aag   1158
Met Gln Leu Met Ser Tyr Pro Leu Ser Glu Gly Gln Leu Asp Gln Lys
            365                 370                 375

aca gcc atg tca ctc ctg tgg aag tcc tat ccc ctt gtt tgc att gct   1206
Thr Ala Met Ser Leu Leu Trp Lys Ser Tyr Pro Leu Val Cys Ile Ala
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aag gaa ctg att cca gaa gcc act gag aaa tac tta gga gga aca gac   1254
Lys Glu Leu Ile Pro Glu Ala Thr Glu Lys Tyr Leu Gly Gly Thr Asp
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gac act gtc aaa aag aaa gac ctg ttc ctg gac ttg ata gca gat gtg   1302
Asp Thr Val Lys Lys Lys Asp Leu Phe Leu Asp Leu Ile Ala Asp Val
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atg ttt ggt gtc cca tct gtg att gtg gcc cgg aac cac aga gat gct   1350
Met Phe Gly Val Pro Ser Val Ile Val Ala Arg Asn His Arg Asp Ala
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Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln Tyr Arg Pro Ser Phe Ser
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tca gac atg aaa ccc aag acg gtg ata gga gac cac ggg gat gag ctc   1446
Ser Asp Met Lys Pro Lys Thr Val Ile Gly Asp His Gly Asp Glu Leu
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ttc tcc gtc ttt ggg gcc cca ttt tta aaa gag ggt gcc tca gaa gag   1494
Phe Ser Val Phe Gly Ala Pro Phe Leu Lys Glu Gly Ala Ser Glu Glu
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gag atc aga ctt agc aag atg gtg atg aaa ttc tgg gcc aac ttt gct   1542
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Arg Asn Gly Asn Pro Asn Gly Glu Gly Leu Pro His Trp Pro Glu Tyr
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aac cag aag gaa ggg tat ctg cag att ggt gcc aac acc cag gcg gcc 1638
Asn Gln Lys Glu Gly Tyr Leu Gln Ile Gly Ala Asn Thr Gln Ala Ala
525 530 535

cag aag ctg aag gac aaa gaa gta gct ttc tgg acc aac ctc ttt gcc 1686
Gln Lys Leu Lys Asp Lys Glu Val Ala Phe Trp Thr Asn Leu Phe Ala
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aag aag gca gtg gag aag cca ccc cag aca gaa cac ata gag ctg tga 1734
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ctcctacc atg tgc ctc tct gct ctg atc ctg gtg tca ctt gca gca ttc 170
Met Cys Leu Ser Ala Leu Ile Leu Val Ser Leu Ala Ala Phe
1 5 10

aca gca ggg gca gga cat cca tcc tca cca ccc atg gtg gac acc gtg 218
Thr Ala Gly Ala Gly His Pro Ser Ser Pro Pro Met Val Asp Thr Val
15 20 25 30

caa ggc aaa gtc ctg ggg aag tac atc agc tta gaa gga ttc aca cag 266
Gln Gly Lys Val Leu Gly Lys Tyr Ile Ser Leu Glu Gly Phe Thr Gln
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Pro Val Ala Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly
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Ser Leu Arg Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Ser Val
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aag aat gcc acc tcc tac cct cct atg tgc ttc caa gac cca gtg aca   410
Lys Asn Ala Thr Ser Tyr Pro Pro Met Cys Phe Gln Asp Pro Val Thr
    80                  85                  90

ggg caa ata gtc aat gac ctc cta act aac aga aag gag aaa att cct   458
Gly Gln Ile Val Asn Asp Leu Leu Thr Asn Arg Lys Glu Lys Ile Pro
95                  100                 105                 110

ctc cag ttt tct gaa gac tgt ctc tac ctg aat att tac act cca gct   506
Leu Gln Phe Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala
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gac ttg aca aag agt gac aga ttg cca gtg atg gtg tgg atc cat gga   554
Asp Leu Thr Lys Ser Asp Arg Leu Pro Val Met Val Trp Ile His Gly
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ggt gga cta gtg tta ggt ggg gca tca acc tat gat gga ctg gtc ctg   602
Gly Gly Leu Val Leu Gly Gly Ala Ser Thr Tyr Asp Gly Leu Val Leu
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tct acg cat gaa aat gtc gtg gtg gtg gtc atc caa tac cgt ttg ggc   650
Ser Thr His Glu Asn Val Val Val Val Val Ile Gln Tyr Arg Leu Gly
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atc tgg gga ttc ttc agc aca ggg gat gaa cac agc agg ggg aac tgg   698
Ile Trp Gly Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp
175                 180                 185                 190

ggt cac ttg gac cag gtg gct gca cta cac tgg gtc cag gac aac att   746
Gly His Leu Asp Gln Val Ala Ala Leu His Trp Val Gln Asp Asn Ile
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gct aaa ttt gga ggt gac cca ggc tct gtg acc atc ttt gga gag tca   794
Ala Lys Phe Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser
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Ala Gly Gly Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys
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aat ctc ttc cag agg gct att tct gaa agt ggt gtg gcc ctc act gca   890
Asn Leu Phe Gln Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Thr Ala
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ggc ctg gtc aag aag aac acc agg cct ttg gct gag aaa att gct gtc   938
Gly Leu Val Lys Lys Asn Thr Arg Pro Leu Ala Glu Lys Ile Ala Val
255                 260                 265                 270

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Ile Ser Gly Cys Lys Asn Thr Thr Ser Ala Ala Met Val His Cys Leu
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ctt ttt aag ctg gat ttg cat gga gac tcc aga cag agc cat ccc ttt   1082
Leu Phe Lys Leu Asp Leu His Gly Asp Ser Arg Gln Ser His Pro Phe
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gtt ccc act gtg ctt gat gga gtg ttg ctg cca aag atg cct gag gag   1130
Val Pro Thr Val Leu Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu
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atc ctg gct gag aag aac ttc aac aca gtg ccc tac atc gtg gga atc   1178
Ile Leu Ala Glu Lys Asn Phe Asn Thr Val Pro Tyr Ile Val Gly Ile
335                 340                 345                 350

aac aag caa gag ttt ggc tgg att ctg cca act atg atg aac tac cca   1226
Asn Lys Gln Glu Phe Gly Trp Ile Leu Pro Thr Met Met Asn Tyr Pro
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ccc tct gat gta aaa ttg gac cag atg acg gcc atg tct ctc ttg aag   1274
Pro Ser Asp Val Lys Leu Asp Gln Met Thr Ala Met Ser Leu Leu Lys
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aag tcc tct ttt ctt ctt aac ctc cct gag gat gca att gca gtg gcc   1322
Lys Ser Ser Phe Leu Leu Asn Leu Pro Glu Asp Ala Ile Ala Val Ala
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att gag aag tat tta aga gat aaa gat tac aca ggc aga aat aaa gac   1370
Ile Glu Lys Tyr Leu Arg Asp Lys Asp Tyr Thr Gly Arg Asn Lys Asp
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caa ctt ctg gaa ttg att ggg gat gtg gta ttc ggt gta cca tct gtg   1418
Gln Leu Leu Glu Leu Ile Gly Asp Val Val Phe Gly Val Pro Ser Val
415                 420                 425                 430

att gtg tcc cgt gga cat aga gat gcc gga gcc ccc aca tac atg tat   1466
Ile Val Ser Arg Gly His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr
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gag ttt caa tat agt cca agc ttc tcg tca gaa atg aaa cca gat acg   1514
Glu Phe Gln Tyr Ser Pro Ser Phe Ser Ser Glu Met Lys Pro Asp Thr
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gtg gta gga gac cat gga gat gaa atc tac tct gtc ttt ggg gcc cca   1562
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att tta aga ggt ggt acc tca gaa gag gag atc aac ctc agc aag atg   1610
Ile Leu Arg Gly Gly Thr Ser Glu Glu Glu Ile Asn Leu Ser Lys Met
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atg atg aaa ttc tgg gcc aac ttt gct agg aat ggg aat ccc aat gga   1658
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cac act gag ctg tga atgggagact ctgtcagcct caccctcagg ggagcccaaa 1857
His Thr Glu Leu
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